

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1552	west adj nile	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/06/09 15:43
L2	231063	conserv\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/06/09 15:44
L3	11569	capsid	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/06/09 15:44
L4	164	I1 and I2 and I3	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/06/09 15:44



results of BLAST

BLASTN 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1149884911-10709-74675597701.BLASTQ1

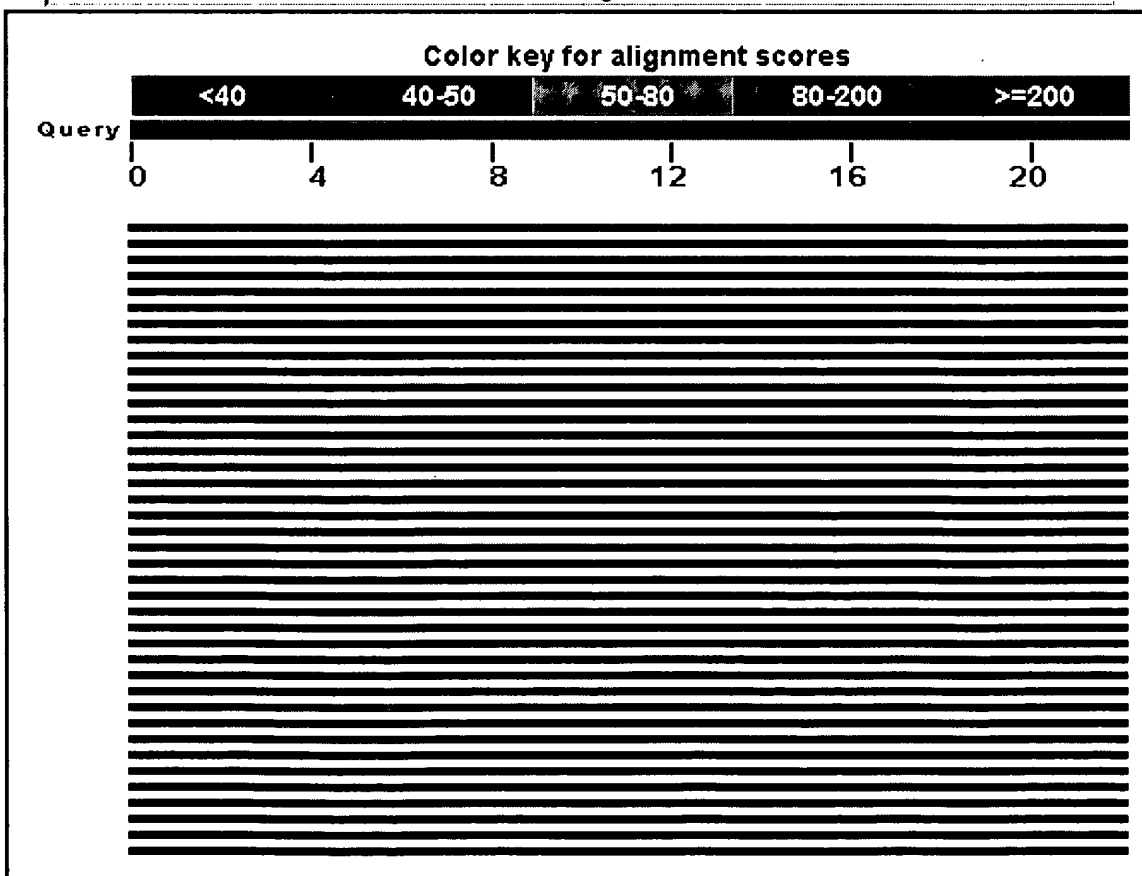
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
3,946,763 sequences; 17,323,791,715 total letters

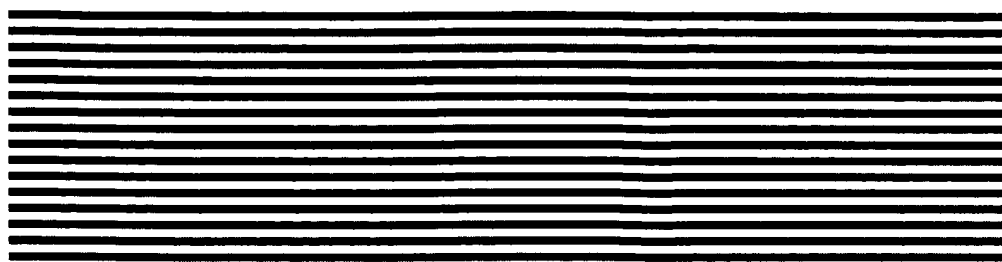
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=22

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments





Tree view 

Sequences producing significant alignments:			Score (Bits)	E Value
gi 55975602 gb AY660002.1 	West Nile virus isolate Mex03 from Me		44.1	0.004
gi 55495180 gb AY712948.1 	West Nile virus isolate Mosquito v436		44.1	0.004
gi 55495165 gb AY712947.1 	West Nile virus isolate Bird 1461, co		44.1	0.004
gi 55495149 gb AY712946.1 	West Nile virus isolate Bird 1171, co		44.1	0.004
gi 55495130 gb AY712945.1 	West Nile virus isolate Bird 1153, co		44.1	0.004
gi 51095221 gb AY688948.1 	West Nile virus strain Sarafend, comp		44.1	0.004
gi 77980183 gb AY848696.2 	West Nile virus strain 385-99 isol...		44.1	0.004
gi 77980181 gb AY848695.2 	West Nile virus strain 385-99 isol...		44.1	0.004
gi 77853218 gb AY848697.2 	West Nile virus strain 385-99 isol...		44.1	0.004
gi 66735926 gb DQ066423.1 	West Nile virus strain 385-99 isol...		44.1	0.004
gi 75859185 gb AY842931.3 	West Nile virus strain 385-99, comple		44.1	0.004
gi 77166600 gb DQ211652.1 	West Nile virus strain NY99, complete		44.1	0.004
gi 33242576 gb AY268133.1 	West Nile virus strain PaH001 poly...		44.1	0.004
gi 89148117 gb DQ118127.1 	West Nile virus isolate goose-Hungary		44.1	0.004
gi 21929238 gb AF404756.1 	West Nile virus isolate WN NY 2000-cr		44.1	0.004
gi 21929236 gb AF404755.1 	West Nile virus isolate WN NY 2000-gr		44.1	0.004
gi 21929234 gb AF404754.1 	West Nile virus isolate WN NJ 2000 MQ		44.1	0.004
gi 21929232 gb AF404753.1 	West Nile virus isolate WN MD 2000-cr		44.1	0.004
gi 19387527 gb AF481864.1 	West Nile virus strain IS-98 STD, com		44.1	0.004
gi 89340786 gb DQ411035.1 	West Nile virus isolate Ast02-2-692,		44.1	0.004
gi 89340784 gb DQ411034.1 	West Nile virus isolate Ast02-2-691,		44.1	0.004
gi 89340782 gb DQ411033.1 	West Nile virus isolate Ast02-3-165,		44.1	0.004
gi 89340780 gb DQ411032.1 	West Nile virus isolate Ast02-3-146,		44.1	0.004
gi 89340778 gb DQ411031.1 	West Nile virus isolate Ast01-187, co		44.1	0.004
gi 89340495 gb DQ411030.1 	West Nile virus isolate Ast01-182, co		44.1	0.004
gi 89340493 gb DQ411029.1 	West Nile virus isolate Ast01-66, com		44.1	0.004
gi 19421851 gb AF375044.1 	West Nile virus isolate WN_0247 polyp		44.1	0.004
gi 19421847 gb AF375042.1 	West Nile virus isolate WN_0043 polyp		44.1	0.004
gi 17226060 gb AF375223.1 	AF375223 West Nile virus polyprotein g		44.1	0.004
gi 87116126 gb DQ377180.1 	West Nile virus isolate Ast02-3-208,		44.1	0.004
gi 87116124 gb DQ377179.1 	West Nile virus isolate Ast02-2-298,		44.1	0.004
gi 87116122 gb DQ377178.1 	West Nile virus isolate Ast02-2-26, c		44.1	0.004
gi 87083864 gb DQ374653.1 	West Nile virus isolate Ast02-2-25, c		44.1	0.004
gi 87083862 gb DQ374652.1 	West Nile virus isolate Ast04-2-824A,		44.1	0.004
gi 87083860 gb DQ374651.1 	West Nile virus isolate Ast02-3-570,		44.1	0.004
gi 87083858 gb DQ374650.1 	West Nile virus isolate Ast02-3-717,		44.1	0.004
gi 30349729 gb AY278441.1 	West Nile virus isolate Ast99-901, co		44.1	0.004
gi 51318183 gb AY603654.1 	West Nile virus strain EthAn4766, com		44.1	0.004
gi 55669121 gb AY646354.1 	West Nile virus from USA, complete ge		44.1	0.004
gi 50872125 dbj AB185915.2 	West Nile virus gene for polyprot...		44.1	0.004
gi 50872124 dbj AB185914.2 	West Nile virus gene for polyprot...		44.1	0.004
gi 50838784 dbj AB185917.1 	West Nile virus gene for polyprot...		44.1	0.004
gi 50838782 dbj AB185916.1 	West Nile virus gene for polyprot...		44.1	0.004
gi 11597239 gb AF196835.2 	AF196835 West Nile virus strain NY99-f		44.1	0.004

gi 71483642 gb DQ080072.1 	West Nile virus isolate FL232 poly...	44.1	0.004
gi 71483640 gb DQ080071.1 	West Nile virus isolate FL234 poly...	44.1	0.004
gi 71483638 gb DQ080070.1 	West Nile virus isolate TVP9115 po...	44.1	0.004
gi 71483636 gb DQ080069.1 	West Nile virus isolate TVP9117 po...	44.1	0.004
gi 71483634 gb DQ080068.1 	West Nile virus isolate TVP9218 po...	44.1	0.004
gi 71483632 gb DQ080067.1 	West Nile virus isolate TVP9219 po...	44.1	0.004
gi 71483630 gb DQ080066.1 	West Nile virus isolate TVP9220 po...	44.1	0.004
gi 71483628 gb DQ080065.1 	West Nile virus isolate TVP9221 po...	44.1	0.004
gi 71483626 gb DQ080064.1 	West Nile virus isolate TVP9222 po...	44.1	0.004
gi 71483624 gb DQ080063.1 	West Nile virus isolate TVP9223 po...	44.1	0.004
gi 71483622 gb DQ080062.1 	West Nile virus isolate TWN165 pol...	44.1	0.004
gi 71483620 gb DQ080061.1 	West Nile virus isolate TWN496 pol...	44.1	0.004
gi 71483618 gb DQ080060.1 	West Nile virus isolate WNVcc poly...	44.1	0.004
gi 71483616 gb DQ080059.1 	West Nile virus isolate L-CA-04 SA...	44.1	0.004
gi 71483614 gb DQ080058.1 	West Nile virus isolate J-CA-03 Ar...	44.1	0.004
gi 71483612 gb DQ080057.1 	West Nile virus isolate I-CA-03 Ar...	44.1	0.004
gi 71483610 gb DQ080056.1 	West Nile virus isolate G-CA-03 IM...	44.1	0.004
gi 71483608 gb DQ080055.1 	West Nile virus isolate F-CA-03 IM...	44.1	0.004
gi 71483606 gb DQ080054.1 	West Nile virus isolate E-CA-03 GR...	44.1	0.004
gi 71483604 gb DQ080053.1 	West Nile virus isolate C-AZ-03 03...	44.1	0.004
gi 71483602 gb DQ080052.1 	West Nile virus isolate B-AZ-03-16...	44.1	0.004
gi 71483600 gb DQ080051.1 	West Nile virus isolate A-AZ-03-16...	44.1	0.004
gi 9930133 gb AF260967.1 AF260967	West Nile virus strain NY99-eq	44.1	0.004
gi 26284711 gb AF533540.1 	West Nile virus polyprotein precursor	44.1	0.004
gi 77172001 gb AF206518.2 AF206518	West Nile virus isolate 2741,	44.1	0.004
gi 6715269 gb AF194117.1 AF194117	West Nile virus structural pro	44.1	0.004
gi 6581069 gb AF202541.1 AF202541	West Nile virus strain HNY1...	44.1	0.004
gi 33948906 gb AY289214.1 	West Nile virus strain TVP 8533 compl	44.1	0.004
gi 59876232 gb AY795965.1 	West Nile virus isolate ARC10, comple	44.1	0.004
gi 58618098 gb AY839588.1 	West Nile virus strain MgAn 786/6/...	44.1	0.004
gi 76781571 gb DQ164206.1 	West Nile virus isolate TX 2004 Harri	44.1	0.004
gi 76781569 gb DQ164205.1 	West Nile virus isolate TX 2002 2, co	44.1	0.004
gi 76781567 gb DQ164204.1 	West Nile virus isolate CO 2003 1, co	44.1	0.004
gi 76781565 gb DQ164203.1 	West Nile virus isolate CO 2003 2, co	44.1	0.004
gi 76781563 gb DQ164202.1 	West Nile virus isolate OH 2002, comp	44.1	0.004
gi 76781561 gb DQ164201.1 	West Nile virus isolate AZ 2004, comp	44.1	0.004
gi 76781559 gb DQ164200.1 	West Nile virus isolate IN 2002, comp	44.1	0.004
gi 76781557 gb DQ164199.1 	West Nile virus isolate TX 2003, comp	44.1	0.004
gi 76781555 gb DQ164198.1 	West Nile virus isolate TX 2002 1, co	44.1	0.004
gi 76781553 gb DQ164197.1 	West Nile virus isolate GA 2002 2, co	44.1	0.004
gi 76781551 gb DQ164196.1 	West Nile virus isolate GA 2002 1, co	44.1	0.004
gi 76781549 gb DQ164195.1 	West Nile virus isolate NY 2002 Nassa	44.1	0.004
gi 76781547 gb DQ164194.1 	West Nile virus isolate NY 2001 Suffo	44.1	0.004
gi 76781545 gb DQ164193.1 	West Nile virus isolate NY 2002 Clint	44.1	0.004
gi 76781543 gb DQ164192.1 	West Nile virus isolate NY 2003 Rockl	44.1	0.004
gi 76781541 gb DQ164191.1 	West Nile virus isolate NY 2003 Chaut	44.1	0.004
gi 76781539 gb DQ164190.1 	West Nile virus isolate NY 2003 Suffo	44.1	0.004
gi 76781537 gb DQ164189.1 	West Nile virus isolate NY 2003 Alban	44.1	0.004
gi 76781535 gb DQ164188.1 	West Nile virus isolate NY 2003 Westc	44.1	0.004
gi 76781533 gb DQ164187.1 	West Nile virus isolate NY 2002 Broom	44.1	0.004
gi 76781531 gb DQ164186.1 	West Nile virus isolate NY 2002 Queen	44.1	0.004
gi 46277828 gb AY490240.2 	West Nile virus strain Chin-01, compl	42.1	0.014
gi 33242574 gb AY268132.1 	West Nile virus strain PaAn001 pol...	42.1	0.014
gi 30230630 gb AY262283.1 	West Nile virus isolate KN3829 polypr	42.1	0.014
gi 21929240 gb AF404757.1 	West Nile virus isolate WN Italy 1998	42.1	0.014
gi 19421853 gb AF375045.1 	West Nile virus isolate WN_0304 polyp	42.1	0.014

Alignments

[Get selected sequences](#)[Select all](#)[Deselect all](#)[Tree View](#)

> [gi|55975602|gb|AY660002.1|](#) **D** West Nile virus isolate Mex03 from Mexico, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|55495180|gb|AY712948.1|](#) **D** West Nile virus isolate Mosquito v4369, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

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Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|55495165|gb|AY712947.1|](#) **D** West Nile virus isolate Bird 1461, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|55495149|gb|AY712946.1|](#) **D** West Nile virus isolate Bird 1171, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|55495130|gb|AY712945.1|](#) **D** West Nile virus isolate Bird 1153, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
```

Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|51095221|gb|AY688948.1| **D** West Nile virus strain Sarafend, complete genome
Length=11057

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|77980183|gb|AY848696.2| **D** West Nile virus strain 385-99 isolate hamster passage
9317E, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|77980181|gb|AY848695.2| **D** West Nile virus strain 385-99 isolate hamster passage
9317A, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|77853218|gb|AY848697.2| **D** West Nile virus strain 385-99 isolate hamster passage
TVP-9376, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|66735926|gb|DQ066423.1| **D** West Nile virus strain 385-99 isolate hamster passage
9317B, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)

. Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|75859185|gb|AY842931.3|](#) **D** West Nile virus strain 385-99, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|77166600|gb|DQ211652.1|](#) **D** West Nile virus strain NY99, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|33242576|gb|AY268133.1|](#) **D** West Nile virus strain PaH001 polyprotein (pol) gene,
cds
Length=10989

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 175    AGCCCTCTTCAGTCCAATCAAG  154
```

> [gi|89148117|gb|DQ118127.1|](#) **D** West Nile virus isolate goose-Hungary/03, complete ger
Length=10969

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```
Query 1      AGCCCTCTTCAGTCCAATCAAG  22
            |||
Sbjct 195    AGCCCTCTTCAGTCCAATCAAG  174
```

> [gi|21929238|gb|AF404756.1|](#) **D** West Nile virus isolate WN NY 2000-crow3356, complete
Length=11029

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|21929236|gb|AF404755.1| **D** West Nile virus isolate WN NY 2000-grouse3282, complete
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|21929234|gb|AF404754.1| **D** West Nile virus isolate WN NJ 2000 MQ5488, complete ge
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|21929232|gb|AF404753.1| **D** West Nile virus isolate WN MD 2000-crow265, complete
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|19387527|gb|AF481864.1| **D** West Nile virus strain IS-98 STD, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|89340786|gb|DQ411035.1| **D** West Nile virus isolate Ast02-2-692, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340784|gb|DQ411034.1|](#) **D** West Nile virus isolate Ast02-2-691, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340782|gb|DQ411033.1|](#) **D** West Nile virus isolate Ast02-3-165, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340780|gb|DQ411032.1|](#) **D** West Nile virus isolate Ast02-3-146, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340778|gb|DQ411031.1|](#) **D** West Nile virus isolate Ast01-187, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340495|gb|DQ411030.1|](#) **D** West Nile virus isolate Ast01-182, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|89340493|gb|DQ411029.1|](#) **D** West Nile virus isolate Ast01-66, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|19421851|gb|AF375044.1|](#) West Nile virus isolate WN_0247 polyprotein mRNA, partial
Length=1648

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 26 AGCCCTCTTCAGTCCAATCAAG 5

> [gi|19421847|gb|AF375042.1|](#) West Nile virus isolate WN_0043 polyprotein mRNA, partial
Length=1648

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 26 AGCCCTCTTCAGTCCAATCAAG 5

> [gi|17226060|gb|AF375223.1|AF375223](#) West Nile virus polyprotein gene, partial cds
Length=1648

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 26 AGCCCTCTTCAGTCCAATCAAG 5

> [gi|87116126|gb|DQ377180.1|](#) **D** West Nile virus isolate Ast02-3-208, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> gi|87116124|gb|DQ377179.1| **D** West Nile virus isolate Ast02-2-298, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> gi|87116122|gb|DQ377178.1| **D** West Nile virus isolate Ast02-2-26, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> gi|87083864|gb|DQ374653.1| **D** West Nile virus isolate Ast02-2-25, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> gi|87083862|gb|DQ374652.1| **D** West Nile virus isolate Ast04-2-824A,, complete genome
Length=10789

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> gi|87083860|gb|DQ374651.1| **D** West Nile virus isolate Ast02-3-570, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004

Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|87083858|gb|DQ374650.1](#) **D** West Nile virus isolate Ast02-3-717, complete genome
Length=10811

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 172 AGCCCTCTTCAGTCCAATCAAG 151

> [gi|30349729|gb|AY278441.1](#) **D** West Nile virus isolate Ast99-901, complete genome
Length=10998

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|51318183|gb|AY603654.1](#) **D** West Nile virus strain EthAn4766, complete genome
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|55669121|gb|AY646354.1](#) **D** West Nile virus from USA, complete genome
Length=11030

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|50872125|dbj|AB185915.2](#) **D** West Nile virus gene for polyprotein precursor prote:
cds, isolate: 6-SP
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|50872124|dbj|AB185914.2|](#) **D** West Nile virus gene for polyprotein precursor protei
cds, isolate: 6-LP
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|50838784|dbj|AB185917.1|](#) **D** West Nile virus gene for polyprotein precursor protei
cds, isolate: B-LP
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|50838782|dbj|AB185916.1|](#) **D** West Nile virus gene for polyprotein precursor protei
cds, isolate: B-SP
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> [gi|11597239|gb|AF196835.2|AF196835](#) **D** West Nile virus strain NY99-flamingo382-99, cc
Length=11029

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 195 AGCCCTCTTCAGTCCAATCAAG 174

> gi|71483642|gb|DQ080072.1| **D** West Nile virus isolate FL232 polyprotein precursor, complete cds
Length=11000

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 166 AGCCCTCTTCAGTCCAATCAAG 145

> gi|71483640|gb|DQ080071.1| **D** West Nile virus isolate FL234 polyprotein precursor, complete cds
Length=11000

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 166 AGCCCTCTTCAGTCCAATCAAG 145

> gi|71483638|gb|DQ080070.1| **D** West Nile virus isolate TVP9115 polyprotein precursor, complete cds
Length=11001

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 167 AGCCCTCTTCAGTCCAATCAAG 146

> gi|71483636|gb|DQ080069.1| **D** West Nile virus isolate TVP9117 polyprotein precursor, complete cds
Length=10975

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1 AGCCCTCTTCAGTCCAATCAAG 22
|||||
Sbjct 167 AGCCCTCTTCAGTCCAATCAAG 146

> gi|71483634|gb|DQ080068.1| **D** West Nile virus isolate TVP9218 polyprotein precursor, complete cds
Length=11001

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```

Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 167    AGCCCTCTTCAGTCCAATCAAG  146

```

> [gi|71483632|gb|DQ080067.1|](#) **D** West Nile virus isolate TVP9219 polyprotein precursor, complete cds
Length=11001

Score = 44.1 bits (22), Expect = 0.004
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```

Query 1      AGCCCTCTTCAGTCCAATCAAG  22
             |||
Sbjct 167    AGCCCTCTTCAGTCCAATCAAG  146

```


Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Jun 5, 2006 10:17 PM

Number of letters in database: 143,922,531

Number of sequences in database: 3,946,763

Lambda K H
1.37 0.711 1.31

Gapped
Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 3946763

Number of Hits to DB: 272830

Number of extensions: 10932

Number of successful extensions: 10932

Number of sequences better than 10: 23

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 10932

Number of HSP's successfully gapped: 23

Length of query: 22

Length of database: 17323791715

Length adjustment: 18

Effective length of query: 4

Effective length of database: 17252749981

Effective search space: 69010999924

Effective search space used: 69010999924

A: 0

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 25 (49.6 bits)

S1: 11 (22.3 bits)

S2: 17 (34.2 bits)



results of BLAST

BLASTN 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1149884457-23746-93944912608.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
3,946,763 sequences; 17,323,791,715 total letters

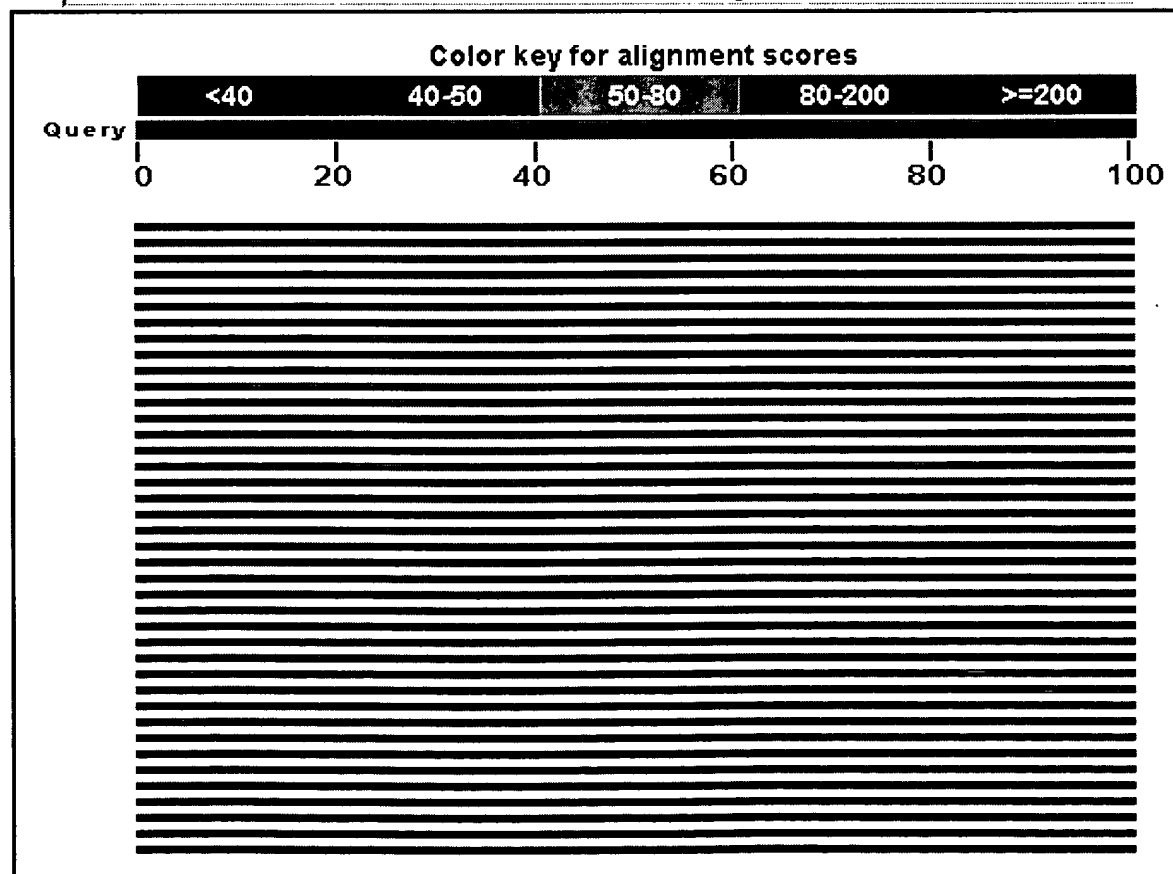
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

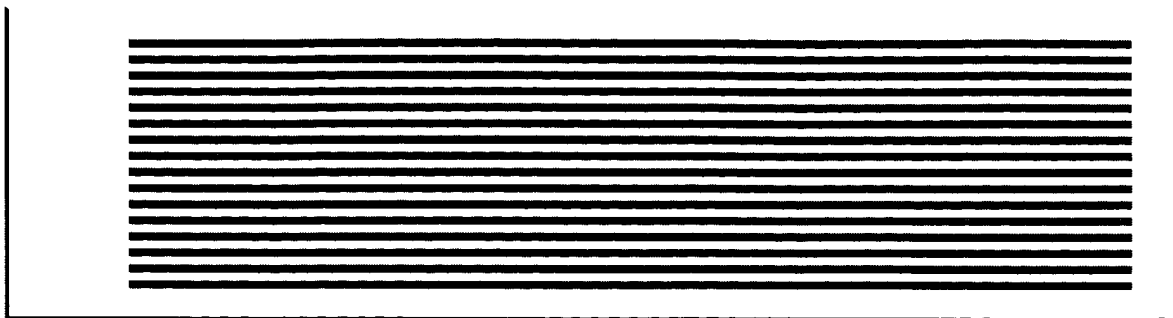
Query=

Length=101

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments





Tree view 

Sequences producing significant alignments:			Score (Bits)	E Value
gi 55975602 gb AY660002.1 	West Nile virus isolate Mex03 from Me		200	5e-49
gi 55495180 gb AY712948.1 	West Nile virus isolate Mosquito v436		200	5e-49
gi 55495165 gb AY712947.1 	West Nile virus isolate Bird 1461, co		200	5e-49
gi 55495149 gb AY712946.1 	West Nile virus isolate Bird 1171, co		200	5e-49
gi 55495130 gb AY712945.1 	West Nile virus isolate Bird 1153, co		200	5e-49
gi 77980183 gb AY848696.2 	West Nile virus strain 385-99 isol...		200	5e-49
gi 77980181 gb AY848695.2 	West Nile virus strain 385-99 isol...		200	5e-49
gi 77853218 gb AY848697.2 	West Nile virus strain 385-99 isol...		200	5e-49
gi 66735926 gb DQ066423.1 	West Nile virus strain 385-99 isol...		200	5e-49
gi 75859185 gb AY842931.3 	West Nile virus strain 385-99, comple		200	5e-49
gi 77166600 gb DQ211652.1 	West Nile virus strain NY99, complete		200	5e-49
gi 46277828 gb AY490240.2 	West Nile virus strain Chin-01, compl		200	5e-49
gi 33242576 gb AY268133.1 	West Nile virus strain PaH001 poly...		200	5e-49
gi 33242574 gb AY268132.1 	West Nile virus strain PaAn001 pol...		200	5e-49
gi 89148117 gb DQ118127.1 	West Nile virus isolate goose-Hungary		200	5e-49
gi 21929240 gb AF404757.1 	West Nile virus isolate WN Italy 1998		200	5e-49
gi 21929238 gb AF404756.1 	West Nile virus isolate WN NY 2000-cr		200	5e-49
gi 21929234 gb AF404754.1 	West Nile virus isolate WN NJ 2000 MQ		200	5e-49
gi 21929232 gb AF404753.1 	West Nile virus isolate WN MD 2000-cr		200	5e-49
gi 19387527 gb AF481864.1 	West Nile virus strain IS-98 STD, com		200	5e-49
gi 30349731 gb AY278442.1 	West Nile virus isolate LEIV-Vlg00-27		200	5e-49
gi 30349727 gb AY277252.1 	West Nile virus isolate LEIV-Vlg99-27		200	5e-49
gi 51318183 gb AY603654.1 	West Nile virus strain EthAn4766, com		200	5e-49
gi 50872125 dbj AB185915.2 	West Nile virus gene for polyprot...		200	5e-49
gi 50872124 dbj AB185914.2 	West Nile virus gene for polyprot...		200	5e-49
gi 50838784 dbj AB185917.1 	West Nile virus gene for polyprot...		200	5e-49
gi 50838782 dbj AB185916.1 	West Nile virus gene for polyprot...		200	5e-49
gi 12744408 gb AF317203.1 AF317203	West Nile virus VLG-4 polypro		200	5e-49
gi 11597239 gb AF196835.2 AF196835	West Nile virus strain NY99-f		200	5e-49
gi 71483642 gb DQ080072.1 	West Nile virus isolate FL232 poly...		200	5e-49
gi 71483640 gb DQ080071.1 	West Nile virus isolate FL234 poly...		200	5e-49
gi 71483638 gb DQ080070.1 	West Nile virus isolate TVP9115 po...		200	5e-49
gi 71483636 gb DQ080069.1 	West Nile virus isolate TVP9117 po...		200	5e-49
gi 71483634 gb DQ080068.1 	West Nile virus isolate TVP9218 po...		200	5e-49
gi 71483632 gb DQ080067.1 	West Nile virus isolate TVP9219 po...		200	5e-49
gi 71483630 gb DQ080066.1 	West Nile virus isolate TVP9220 po...		200	5e-49
gi 71483628 gb DQ080065.1 	West Nile virus isolate TVP9221 po...		200	5e-49
gi 71483626 gb DQ080064.1 	West Nile virus isolate TVP9222 po...		200	5e-49
gi 71483624 gb DQ080063.1 	West Nile virus isolate TVP9223 po...		200	5e-49
gi 71483622 gb DQ080062.1 	West Nile virus isolate TWN165 pol...		200	5e-49
gi 71483620 gb DQ080061.1 	West Nile virus isolate TWN496 pol...		200	5e-49
gi 71483616 gb DQ080059.1 	West Nile virus isolate L-CA-04 SA...		200	5e-49
gi 71483614 gb DQ080058.1 	West Nile virus isolate J-CA-03 Ar...		200	5e-49
gi 71483612 gb DQ080057.1 	West Nile virus isolate I-CA-03 Ar...		200	5e-49

gi 71483610 gb DQ080056.1 	West Nile virus isolate G-CA-03 IM...	200	5e-49
gi 71483608 gb DQ080055.1 	West Nile virus isolate F-CA-03 IM...	200	5e-49
gi 71483606 gb DQ080054.1 	West Nile virus isolate E-CA-03 GR...	200	5e-49
gi 71483604 gb DQ080053.1 	West Nile virus isolate C-AZ-03 03...	200	5e-49
gi 71483602 gb DQ080052.1 	West Nile virus isolate B-AZ-03-16...	200	5e-49
gi 71483600 gb DQ080051.1 	West Nile virus isolate A-AZ-03-16...	200	5e-49
gi 9930137 gb AF260969.1 AF260969	West Nile virus strain RO97-50	200	5e-49
gi 9930135 gb AF260968.1 AF260968	West Nile virus strain Eg101,	200	5e-49
gi 9930133 gb AF260967.1 AF260967	West Nile virus strain NY99-eq	200	5e-49
gi 26284711 gb AF533540.1 	West Nile virus polyprotein precursor	200	5e-49
gi 7717200 gb AF206518.2 AF206518	West Nile virus isolate 2741,	200	5e-49
gi 6581069 gb AF202541.1 AF202541	West Nile virus strain HNY1...	200	5e-49
gi 33948906 gb AY289214.1 	West Nile virus strain TVP 8533 compl	200	5e-49
gi 59876232 gb AY795965.1 	West Nile virus isolate ARC10, comple	200	5e-49
gi 51011375 gb AY701413.1 	West Nile virus strain 04.05 polyprot	200	5e-49
gi 51011373 gb AY701412.1 	West Nile virus strain 96-111 polypro	200	5e-49
gi 76781571 gb DQ164206.1 	West Nile virus isolate TX 2004 Harri	200	5e-49
gi 76781567 gb DQ164204.1 	West Nile virus isolate CO 2003 1, co	200	5e-49
gi 76781565 gb DQ164203.1 	West Nile virus isolate CO 2003 2, co	200	5e-49
gi 76781563 gb DQ164202.1 	West Nile virus isolate OH 2002, comp	200	5e-49
gi 76781561 gb DQ164201.1 	West Nile virus isolate AZ 2004, comp	200	5e-49
gi 76781559 gb DQ164200.1 	West Nile virus isolate IN 2002, comp	200	5e-49
gi 76781557 gb DQ164199.1 	West Nile virus isolate TX 2003, comp	200	5e-49
gi 76781553 gb DQ164197.1 	West Nile virus isolate GA 2002 2, co	200	5e-49
gi 76781551 gb DQ164196.1 	West Nile virus isolate GA 2002 1, co	200	5e-49
gi 76781549 gb DQ164195.1 	West Nile virus isolate NY 2002 Nassa	200	5e-49
gi 76781547 gb DQ164194.1 	West Nile virus isolate NY 2001 Suffo	200	5e-49
gi 76781545 gb DQ164193.1 	West Nile virus isolate NY 2002 Clint	200	5e-49
gi 76781543 gb DQ164192.1 	West Nile virus isolate NY 2003 Rockl	200	5e-49
gi 76781541 gb DQ164191.1 	West Nile virus isolate NY 2003 Chaut	200	5e-49
gi 76781539 gb DQ164190.1 	West Nile virus isolate NY 2003 Suffo	200	5e-49
gi 76781537 gb DQ164189.1 	West Nile virus isolate NY 2003 Alban	200	5e-49
gi 76781535 gb DQ164188.1 	West Nile virus isolate NY 2003 Westc	200	5e-49
gi 76781533 gb DQ164187.1 	West Nile virus isolate NY 2002 Broom	200	5e-49
gi 76781531 gb DQ164186.1 	West Nile virus isolate NY 2002 Queen	200	5e-49
gi 30230630 gb AY262283.1 	West Nile virus isolate KN3829 polypr	192	1e-46
gi 21929236 gb AF404755.1 	West Nile virus isolate WN NY 2000-gr	192	1e-46
gi 89340786 gb DQ411035.1 	West Nile virus isolate Ast02-2-692,	192	1e-46
gi 89340784 gb DQ411034.1 	West Nile virus isolate Ast02-2-691,	192	1e-46
gi 89340780 gb DQ411032.1 	West Nile virus isolate Ast02-3-146,	192	1e-46
gi 89340778 gb DQ411031.1 	West Nile virus isolate Ast01-187, co	192	1e-46
gi 89340495 gb DQ411030.1 	West Nile virus isolate Ast01-182, co	192	1e-46
gi 89340493 gb DQ411029.1 	West Nile virus isolate Ast01-66, com	192	1e-46
gi 87116126 gb DQ377180.1 	West Nile virus isolate Ast02-3-208,	192	1e-46
gi 87116124 gb DQ377179.1 	West Nile virus isolate Ast02-2-298,	192	1e-46
gi 87116122 gb DQ377178.1 	West Nile virus isolate Ast02-2-26, c	192	1e-46
gi 87083864 gb DQ374653.1 	West Nile virus isolate Ast02-2-25, c	192	1e-46
gi 87083862 gb DQ374652.1 	West Nile virus isolate Ast04-2-824A,	192	1e-46
gi 87083860 gb DQ374651.1 	West Nile virus isolate Ast02-3-570,	192	1e-46
gi 87083858 gb DQ374650.1 	West Nile virus isolate Ast02-3-717,	192	1e-46
gi 30349729 gb AY278441.1 	West Nile virus isolate Ast99-901, co	192	1e-46
gi 55669121 gb AY646354.1 	West Nile virus from USA, complete ge	192	1e-46
gi 71483618 gb DQ080060.1 	West Nile virus isolate WNVCC poly...	192	1e-46
gi 76781569 gb DQ164205.1 	West Nile virus isolate TX 2002 2, co	192	1e-46
gi 76781555 gb DQ164198.1 	West Nile virus isolate TX 2002 1, co	192	1e-46
gi 89340782 gb DQ411033.1 	West Nile virus isolate Ast02-3-165,	184	3e-44

Alignments

Get selected sequences

Select all

Deselect all

Tree View

> [gi|55975602|gb|AY660002.1|](#) **D** West Nile virus isolate Mex03 from Mexico, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|55495180|gb|AY712948.1|](#) **D** West Nile virus isolate Mosquito v4369, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|55495165|gb|AY712947.1|](#) **D** West Nile virus isolate Bird 1461, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|55495149|gb|AY712946.1|](#) **D** West Nile virus isolate Bird 1171, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
```

```
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148
Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|55495130|gb|AY712945.1](#) **D** West Nile virus isolate Bird 1153, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148
Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|77980183|gb|AY848696.2](#) **D** West Nile virus strain 385-99 isolate hamster passage
9317E, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148
Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|77980181|gb|AY848695.2](#) **D** West Nile virus strain 385-99 isolate hamster passage
9317A, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148
Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|77853218|gb|AY848697.2](#) **D** West Nile virus strain 385-99 isolate hamster passage
TVP-9376, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|66735926|gb|DQ066423.1](#) **D** West Nile virus strain 385-99 isolate hamster passage 9317B, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|75859185|gb|AY842931.3](#) **D** West Nile virus strain 385-99, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```



> [gi|77166600|gb|DQ211652.1](#) **D** West Nile virus strain NY99, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
```



Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189

>  [gi|46277828|gb|AY490240.2|](#)  West Nile virus strain Chin-01, complete genome
Length=11028

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 89   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148



Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

>  [gi|33242576|gb|AY268133.1|](#)  West Nile virus strain PaH001 polyprotein (pol) gene,
cds
Length=10989

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 69   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 128



Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 129  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 169
```

>  [gi|33242574|gb|AY268132.1|](#)  West Nile virus strain PaAn001 polyprotein (pol) gene,
cds
Length=10989

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 69   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 128

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 129  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 169
```

>  [gi|89148117|gb|DQ118127.1|](#)  West Nile virus isolate goose-Hungary/03, complete genome
Length=10969

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|21929240|gb|AF404757.1|](#) **D** West Nile virus isolate WN Italy 1998-equine, complete
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|21929238|gb|AF404756.1|](#) **D** West Nile virus isolate WN NY 2000-crow3356, complete
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|21929234|gb|AF404754.1|](#) **D** West Nile virus isolate WN NJ 2000 MQ5488, complete ge
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|21929232|gb|AF404753.1|](#) **D** West Nile virus isolate WN MD 2000-crow265, complete c
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|19387527|gb|AF481864.1](#) **D** West Nile virus strain IS-98 STD, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|30349731|gb|AY278442.1](#) **D** West Nile virus isolate LEIV-Vlg00-27924, complete ger
Length=10842

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148



Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|30349727|gb|AY277252.1](#) **D** West Nile virus isolate LEIV-Vlg99-27889, complete ger
Length=10845

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148



Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```


>  [gi|51318183|gb|AY603654.1|](#)  West Nile virus strain EthAn4766, complete genome
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148



Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

>  [gi|50872125|dbj|AB185915.2|](#)  West Nile virus gene for polyprotein precursor protei:
cds, isolate: 6-SP
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148



Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

>  [gi|50872124|dbj|AB185914.2|](#)  West Nile virus gene for polyprotein precursor protei:
cds, isolate: 6-LP
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
             |||
Sbjct 89      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61      AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
             |||
Sbjct 149     AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

>  [gi|50838784|dbj|AB185917.1|](#)  West Nile virus gene for polyprotein precursor protei:
cds, isolate: B-LP
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1      AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
```

```

      |||
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 148
      |||
Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
      |||
```

> [gi|50838782|dbj|AB185916.1](#) **D** West Nile virus gene for polyprotein precursor protei
cds, isolate: B-SP
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```

Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 148
      |||
Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
      |||
```

> [gi|12744408|gb|AF317203.1|AF317203](#) **D** West Nile virus VLG-4 polyprotein precursor, c
Length=10972

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```

Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct  57  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 116
      |||
Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct  117  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 157
      |||
```

> [gi|11597239|gb|AF196835.2|AF196835](#) **D** West Nile virus strain NY99-flamingo382-99, c
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```

Query  1  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct  89  AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGCAAGAGCCGGGCTGTCAATATGCTAA 148
      |||
Query  61  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct  149  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
      |||
```

> [gi|71483642|gb|DQ080072.1](#) **D** West Nile virus isolate FL232 polyprotein precursor, c
cds
Length=11000

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
        |||
Sbjct 60 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 119

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
        |||
Sbjct 120 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 160
```

> [gi|71483640|gb|DQ080071.1|](#) **D** West Nile virus isolate FL234 polyprotein precursor, complete cds
Length=11000

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
        |||
Sbjct 60 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 119

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
        |||
Sbjct 120 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 160
```

> [gi|71483638|gb|DQ080070.1|](#) **D** West Nile virus isolate TVP9115 polyprotein precursor, complete cds
Length=11001

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
        |||
Sbjct 61 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
        |||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483636|gb|DQ080069.1|](#) **D** West Nile virus isolate TVP9117 polyprotein precursor, complete cds
Length=10975

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
        |||
Sbjct 61 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120
```

```
Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483634|gb|DQ080068.1|](#) **D** West Nile virus isolate TVP9218 polyprotein precursor, complete cds
Length=11001

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 61 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483632|gb|DQ080067.1|](#) **D** West Nile virus isolate TVP9219 polyprotein precursor, complete cds
Length=11001

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 61 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483630|gb|DQ080066.1|](#) **D** West Nile virus isolate TVP9220 polyprotein precursor, complete cds
Length=11001

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 61 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 121 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

> [gi|71483628|gb|DQ080065.1|](#) **D** West Nile virus isolate TVP9221 polyprotein precursor, complete cds
Length=10995

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 55   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 114

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 115  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 155
```

>[gi|71483626|gb|DQ080064.1|](#) **D** West Nile virus isolate TVP9222 polyprotein precursor, complete cds
Length=11001

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 61   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 121  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

>[gi|71483624|gb|DQ080063.1|](#) **D** West Nile virus isolate TVP9223 polyprotein precursor, complete cds
Length=10975

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 61   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
          |||
Sbjct 121  AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 161
```

>[gi|71483622|gb|DQ080062.1|](#) **D** West Nile virus isolate TWN165 polyprotein precursor, cds
Length=11001

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
          |||
Sbjct 61   AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 120

Query 61   AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
```

Sbjct 121 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 161

> [gi|71483620|gb|DQ080061.1|](#) **D** West Nile virus isolate TWN496 polyprotein precursor, cds
Length=11000

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 60 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 119
Query 61 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 101
|||||
Sbjct 120 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 160

> [gi|71483616|gb|DQ080059.1|](#) **D** West Nile virus isolate L-CA-04 SAC-04-7168 polyprotein gene, complete cds
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148
Query 61 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 189

> [gi|71483614|gb|DQ080058.1|](#) **D** West Nile virus isolate J-CA-03 Arcadia-S0334814 polyprotein precursor, gene, complete cds
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148
Query 61 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTGTCCTTGATTGGACTGAAG 189

> [gi|71483612|gb|DQ080057.1|](#) **D** West Nile virus isolate I-CA-03 Arcadia-S0331532 polyprotein precursor, gene, complete cds
Length=10956

Score = 200 bits (101), Expect = 5e-49

Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483610|gb|DQ080056.1](#) **D** West Nile virus isolate G-CA-03 IMPR-1075 polyprotein
gene, complete cds
Length=11019

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483608|gb|DQ080055.1](#) **D** West Nile virus isolate F-CA-03 IMPR 102 polyprotein
gene, complete cds
Length=11018

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483606|gb|DQ080054.1](#) **D** West Nile virus isolate E-CA-03 GRLA-1260 polyprotein
gene, complete cds
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
      |||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
      |||
```

Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189

> [gi|71483604|gb|DQ080053.1|](#) **D** West Nile virus isolate C-AZ-03 03-1799 polyprotein p1
gene, complete cds
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483602|gb|DQ080052.1|](#) **D** West Nile virus isolate B-AZ-03-1681 polyprotein precu
complete cds
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

> [gi|71483600|gb|DQ080051.1|](#) **D** West Nile virus isolate A-AZ-03-1623 polyprotein precu
complete cds
Length=11029

Score = 200 bits (101), Expect = 5e-49
Identities = 101/101 (100%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```
Query 1 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 60
|||||
Sbjct 89 AGATCTCGATGTCTAAGAAACCAGGAGGGCCCGGCAAGAGCCGGGCTGTCAATATGCTAA 148

Query 61 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 101
|||||
Sbjct 149 AACGCGGAATGCCCCGCGTGTTCCTTGATTGGACTGAAG 189
```

[Get selected sequences](#)[Select all](#)[Deselect all](#)[Tree View](#)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Jun 5, 2006 10:17 PM
Number of letters in database: 143,922,531
Number of sequences in database: 3,946,763
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 3946763
Number of Hits to DB: 1139647
Number of extensions: 51199
Number of successful extensions: 13183
Number of sequences better than 10: 46
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 13183
Number of HSP's successfully gapped: 46
Length of query: 101
Length of database: 17323791715
Length adjustment: 21
Effective length of query: 80
Effective length of database: 17240909692
Effective search space: 1379272775360
Effective search space used: 1379272775360
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)